Clean Copy of Amended Claims

1. (Amended) A method of identifying the nucleotide sequence of a nucleic acid comprising:

loading a first sequencing reaction product at a first loading time into one or more lanes of a sequencing gel;

loading a second short sequencing reaction product onto the same one or more lanes of the sequencing gel as the first short sequencing reaction product at a second loading time, wherein the first loading time and the second loading time are sufficiently temporally separated to separate the first sequencing reaction product from the second sequencing reaction product by electrophoresis; and

performing gel or capillary electrophoresis on the first short sequencing reaction product and on the second short sequencing reaction.

2. (Amended) The method of claim 1, wherein the first sequencing reaction product is produced from a region comprising a SNP (single nucleotide polymorphism).

3. (Amended) The method of claim 1, wherein the first sequencing reaction product is produced from an EST (expressed sequence tag).

4. (Amended) The method of claim 1, wherein the first short sequencing reaction product and second short sequencing reaction product are each about 20 bases or shorter.

5. (Amended) The method of claim 1, wherein the first short sequencing reaction product is a run off sequencing reaction product.

6. (Amended) A method of determining the nucleotide sequence of a portion of a nucleic acid comprising:

a) isolating the nucleic acid from a nucleic acid library wherein the library comprises a recognition site of an enzyme that cuts at least 1 base downstream of the recognition site, wherein the recognition site is positioned within 1 base of an insert of the library;

b) amplifying the nucleic acid;

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c) digesting the amplified nucleic acid with the enzyme;

d) performing a run-off sequencing reaction utilizing a primer that hybridizes to a region of the amplified fragment at or upstream of the recognition site to form a first sequencing reaction product;

e) loading a first sequencing reaction product at a first loading time into one or more lanes of an electrophoresis sequencing device; and f) performing electrophoresis analysis on the first sequencing reaction product.

7. (Amended) The method of claim 6, further comprising the steps of g) loading a second sequencing reaction product onto the same one or more lanes of the electrophoresis sequencing device as the first sequencing reaction product at a second loading time, wherein the first loading time and the second loading time are sufficiently temporally separated to separate the first sequencing reaction product from the second sequencing reaction product by electrophoresis; h) and performing electrophoresis analysis on the second sequencing reaction product.

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8. (Amended) The method of claim 6, wherein the enzyme is a restriction enzyme.

9. (Amended) The method of claim 8, wherein the restriction enzyme is BpmL

10. (Amended) The method of claim 6, wherein the electrophoresis performed is gel electrophoresis.

11. (Amended) The method of claim 6, wherein the electrophoresis is performed with a capillary apparatus.

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14. (New) A method of determining the nucleotide sequence of a portion of a nucleic acid comprising:

a) isolating the nucleic acid from a nucleic acid library wherein the library comprises a recognition site of an enzyme that cuts at least 1 base

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downstream of the recognition site, wherein the recognition site is positioned within 1 base of an insert of the library;

b) amplifying the nucleic acid;

c) digesting the amplified nucleic acid with the enzyme;

d) performing a run-off sequencing reaction utilizing a primer that hybridizes to a region of the amplified fragment at or upstream of the recognition site to form a first sequencing reaction product; and

e) performing mass spectrophotometry on the first sequencing reaction product.

REMARKS

In section 2 of the Office Action, the Examiner notes that the application fails to comply with the requirements of CFR 1.821 through 1.825 for the reasons set forth on the Notice to Comply With Requirements for Patent Applications Containing Nucleotide Sequence and Amino Acid Sequence Disclosures. Enclosed is a copy of the Notice. Per the requirements of the Notice, the Applicants have provided an initial paper copy of the Sequence Listing, a computer readable copy of the Sequence Listing, neither of which contain any new matter with respect to the application as originally filed, and a Statement to Support.

In section 3, the examiner notes that the specification recites sequences that lack description by a sequence identifier set forth in the Sequence Listing. Applicants have amended page 5 to provide the required description.

In section 4, the Examiner states that figures for the application were not provided by the Applicants or the receiving office. Copies of the figures which were filed in PCT Application No. PCT/US99/21092 on November 2, 1999, in response to the Notice to Correct Defects, are enclosed herewith.

35 USC 112 second paragraph

In sections 5 and 6 the Examiner rejects claims 1-13 under 35 USC 112 second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicants regard as the invention.

The Office Action rejects claims 1-5 as being indefinite for failing to recite a final process step that clearly relates back to the preamble and for the recitation of the